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SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Ding, Shou-wei
 - (ii) TITLE OF INVENTION: DISEASE RESISTANT TRANSGENIC PLANTS
 - (iii) NUMBER OF SEQUENCES: 4
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Rothwell, Figg, Ernst & Kurz
 - (B) STREET: 555 Thirteenth Street, N.W., Suite 701 East
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA (F) ZIP: 20004
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible

 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: Patentin Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Figg, Edward A.
 - (B) REGISTRATION NUMBER: 27,195
 - (C) REFERENCE/DOCKET NUMBER: 2248-108
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-783-6040
 - (B) TELEFAX: 202-783-6031
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tomato aspermy virus
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pTMV-30B
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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accettaaga	agaagaagaa	TGGCAAGCAT	CGAGATCCCT	CTACACGAGA	TCATTCGAAA	60
GTTGGAACGG	atgaatcaaa	AGAAACAAGC	ACAGAGGAAA	CGACACAAAC	TGAACCGCAA	120
GGAGCGGGGT	CACAAAAGTC	CAAGTGAACA	AAGGCGATCG	CACTTATGGC	ACGCGCGTCA	180
agttgaactt	TCTGCCATTA	ATTCCGATAA	TTCTTCAGAT	CACCCTACCA	CTCTGTGTCG	240
CTTTGACACA	TTTGGTTÇCA	agtctgatgc	TATTTGTGAT	CGCTCTGACT	GGTGTCTCGA	300

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(2) INFORMATION FOR SEQ ID NO:2:

TCAATGATTT CCGACCCTTC GTCGTCCG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tomato aspermy virus
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pTAVd2bl
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

accettaaga	agaagtagaa	TGTAAAGCAT	CGAGATCCCT	CTACACGAGA	TCATTCGAAA	60
GTTGGAACGG	atgaatcaaa	AGAAACAAGC	ACAGAGGAAA	CGACACAAAC	TGAACCGCAA	120
GGAGCGGGGT	CACAAAAGTC	CAAGTGAACA	AAGGCGATCG	GAGTTATGGC	ACGCGCGTCA	180
AGTTGAACTT	TCTGCCATTA	ATTCCGATAA	TTCTTCAGAT	GAGGGTACCA	CTCTGTGTCG	240
CTTTGACACA	TTTGGTTCCA	AGTCTGATGC	TATTTGTGAT	CGCTCTGACT	GGTGTCTCGA	300
TCAATGATTT	CCGACCCTTC	CTCGTCCG				328

- (2) INFORMATION FOR SEQ ID NO: 3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
 - (111) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:

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(A)	ORGANISM:	Tomato	aspermy	virus

(vii) IMMEDIATE SOURCE: (B) CLONE: pTAVd2b2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCETTAAGA AGAAGTAGAA TETAAAGCAT CGAGATCCCT CTACACGAGA TCATTCGAAA 60
GTTGGAACGG ATGAATCAAA AGAAACAAGC ACAGAGGAAA CGACACAAAC TGAACCGCAA 120
GGAGCGGGGT CACAAAAGTC CAAGTGAATA AAGGTGATCG GAGTTATGGC ACGCGCGTCA 180
AGTTGAACTT TCTGCCATTA ATTCCGATAA TTCTTCAGAT GAGGGTACCA CTCTGTGTCG 240
CTTTGACACA TTTGGTTCCA ACTCTGATGC TATTTGTGAT CGCTCTGACT GGTGTCTCGA 300
TCAATGATTT CCGACCCTTC GTCGTCCG 328

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Cucumber mosaic virus
- (vii) IMMEDIATE SOURCE: (B) CLONE: pCMV2b

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCATGGA	TGTGTTGACA	GTAGTGGTGT	CGACCGCCGA	CCTCCACTTA	GCCAATTTGC	60
AGGAGGTGAA	ACGTCGAAGA	CGAAGGTCTC	ACGTCAGAAA	CCGGCGAGCG	AGGGGTTACA	120
AAAGTCCCAG	CGAGAGAGCG	CGATCTATAG	CGAGACTTTT	CCAGATGTTA	CCATTCCACG	180
GAGTAGATCC	CGTGGATTGG	TTTCCTGATG	TCGTTCGCTC	TCCGTCCGTT	ACCAGCCTTG	240
TTTCTTATGA	atcttttgat	GATACTGATT	GGTTTGCTGG	TAACGAATGG	GCCGAAGGGT	300
CGTTTTGATT	TCCGACCCTT	CCTCCTCCGA	AGACGTTAAA	CTACGCTCTC	TTTATTGCGA	360
GTGCTGAGTT	GGTAGTTTGC	TCTAAACTAT	CTGAAGTCGC	TAAATCCATT	ACTGGTTGCG	420
AACGGGTTGT	CCATCCAGCT	TACGGCTANA	ATGGTCAGTC	ATGCCCCAAA	GGCATGCCGA	480
CACCCTACAG	GGTTGTCGAG	GTAC				504